## Molecular responses in decitabine- and decitabine/ venetoclax-treated patients with acute myeloid leukemia and myelodysplastic syndromes

## Authors

Agata Gruszczynska,<sup>1</sup> Abhishek Maiti,<sup>2</sup> Christopher A. Miller,<sup>1</sup> Sai Mukund Ramakrishnan,<sup>1</sup> Daniel C. Link,<sup>1</sup> Geoffrey L. Uy,<sup>1</sup> Allegra A. Petti,<sup>3</sup> Kala Hayes,<sup>2</sup> Courtney D. DiNardo,<sup>2</sup> Farhad Ravandi,<sup>2</sup> Timothy J. Ley,<sup>1</sup> David H. Spencer,<sup>4</sup> Feng Gao,<sup>5</sup> Marina Y. Konopleva<sup>6</sup> and John S. Welch<sup>1°</sup>

<sup>1</sup>Department of Medicine, Division of Oncology, Washington University School of Medicine, St. Louis, MI; <sup>2</sup>Department of Leukemia, MD Anderson Cancer Center, Houston, TX; <sup>3</sup>Department of Neurosurgery, Washington University School of Medicine, St. Louis, MI; <sup>4</sup>Department of Pathology, Washington University School of Medicine, St. Louis, MO; <sup>5</sup>Department of Surgery, Division of Public Health Sciences, Washington University School of Medicine, St. Louis, MI and <sup>6</sup>Albert Einstein College of Medicine, Bronx, NY, USA

°Current address: A2 Biotherapeutics, Agoura Hills, CA, USA

Correspondence: J.S. WELCH - jwelch@a2biotherapeutics.com

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Α.

## B.



## C.

1035-BM Adj R2 = 0.085467 Intercept = 0.092973 Slope = -0.00043757 P = 0.18487 1.00 Variant Allele Frequency 0.22 0.50 NDH2 DH2 0.00 IDH2 ASXL1 ASXL1 SRSF2 ASXI 1 50 Day 25 75 100





F.



Decitabine/Venetoclax

G.

Decitabine







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6523072-BM Adj R2 = 0.96228 Intercept = 0.43298 Slope = -0.018758 P = 9.7367e-32 1.00 Variant Allele Frequency 0.22 0.22 MT34 PM1D DNMT3A NMŤЗA NRAS 25 0.00 PPM1D NRAS 100 75 0 Day

Supplemental Figure 1



Supplemental Figure2





**Supplemental Figure 4** 

**Supplemental Figure 1**. Representative calculations of molecular responses. A-F. Single-agent decitabine cases with stable disease. D-F. Single-agent decitabine cases with stable disease during the first 1-2 cycles followed by molecular response. G-I. Decitabine/venetoclax cases. Note responses after the first cycle.

**Supplemental Figure 2**. Molecular subgroup analysis. A-C. Comparison of tumor burden and molecular responses measured in BM and PB substrates from patients with MDS and sAML. D-E. Comparison of molecular responses within morphologic responses. One-way ANOVA with Dunn's multiple comparison. F-G. Comparison of molecular responses within de novo AML patients comparing CR vs. other responders (e.g. CRi/mLFS). One-way ANOVA with Dunn's multiple comparison.

**Supplemental Figure 3**. Clinical subgroup analysis. A-F. Impact of clinical features on overall survival within the total cohort of patients (n=95). G-H. Impact of adverse risk karyotypes within treatment cohorts. Log-rank comparisons.

**Supplemental Figure 4.** Subgroup analysis of overall survival based on treatment and the presence of specific gene mutations.